

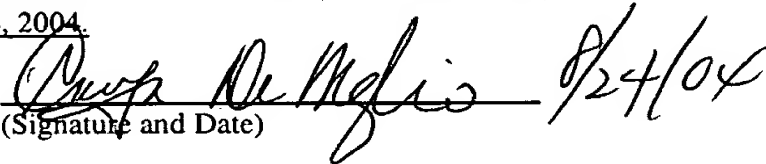
IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICANTS : Michael Meyrick Burrell et al.
SERIAL NO. : 09/383,579
FILED : August 25, 1999
FOR : MODIFICATION OF PLANT FIBRES

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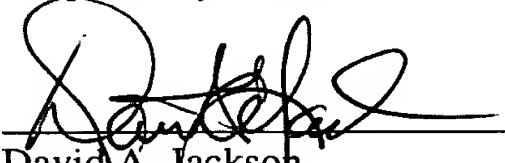
Applicant hereby petitions for grant of priority of the present Application on the basis of the following prior filed foreign Application:

<u>COUNTRY</u>	<u>SERIAL NO.</u>	<u>FILING DATE</u>
GREAT BRITAIN	9818808.9	AUGUST 29, 1998

To perfect Applicant's claim to priority, a certified copy of the above listed prior filed Application is enclosed.

Acknowledgment of Applicant's perfection of claim to priority is accordingly requested.

Respectfully submitted,


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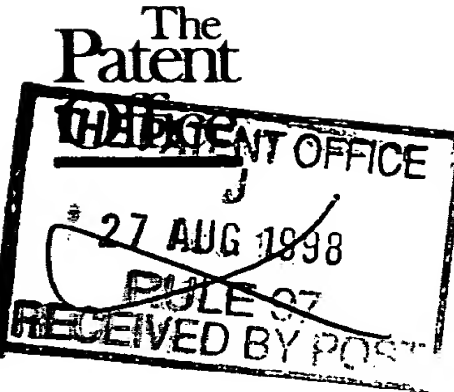
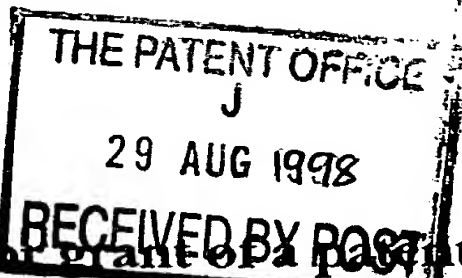
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Advanced Technologies (Cambridge) Limited
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Patents ADP number (if you know it)

If the applicant is a corporate body, give the country/state of its incorporation

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04458832002

4. Title of the invention

MODIFICATION OF PLANT FIBRES

5. Name of your agent (if you have one)

"Address for service" in the United Kingdom to which all correspondence should be sent (including the postcode)

Mrs. M.R. Walford / K.J.H. MacLean
Patents Department
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R&D Centre
Regents Park Road
Southampton SO15 8TL
England

Patents ADP number (if you know it)

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6. If you are declaring priority from one or more earlier patent applications, give the country and the date of filing of the or of each of these earlier applications and (if you know it) the or each application number

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Margot Ruth Walford

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Modification of Plant Fibres

This invention relates to the modification of the morphology of plant fibre cells. The invention is exemplified by methods of using genetic constructs for the modification of, in particular, but not exclusively, *Eucalyptus* fibres, for example.

The primary product of the forestry industry is considered to be wood, although more fundamentally it could be defined as fibre. The industry supplies a wide range of feedstocks to the solid wood and pulp/paper industries who produce a multiplicity of products. The forester must therefore seek to cater for the competing needs of these industries, and even within the individual industries, there is a range of different requirements. For example, different paper grades require different qualities in the starting material.

Forestry-based operations depend upon a balance between the capability of the forester to supply the processor with fibre having specific properties, and the ability of the processor to modify his process and so accommodate the available feedstock. The design and operation of processing plants are influenced by the wood (fibre) properties of the feedstock.

Notwithstanding these specific demands, fibre uniformity and strength are common requirements for most industrial uses,

and hence the fibre supplied by the forester must be capable of delivering these properties to the processor.

In pulp manufacture, for example, strength characteristics are determined in part by fibre length. Increased fibre length leads to the production of paper with increased strength. Bond strength is attributed to contact between the fibres and the adhesion capabilities of the surfaces, which are dependent upon fibre length, perimeter and coarseness. Also, during the manufacturing process, increased fibre length increases the strength of wet webs enabling easier handling (Seth, 1995).

However, long fibres are not desirable for all applications. In some cases, shorter fibres are preferable, such as in the production of smooth-surfaced papers.

Fibre properties differ between species, and consequently particular species have been limited historically to particular applications. Fibres from hardwood species are generally much shorter than those from softwoods. This results in the production of pulp and paper with desirable surface characteristics such as smoothness and brightness, but with low strength characteristics. In practice, where a single species providing fibre with an appropriate combination of characteristics has not been available, the mixing of long and short fibres from different species is used. If a single source were available, possessing the desirable characteristics plus optimal fibre length, this would be of great benefit to the processor. Some common species and their fibre lengths are exemplified in Table 1 below.

Table 1Fibre Lengths of Various Tree Species

Species	Fibre Length (mm)
Loblolly Pine	3.5 - 4.5
Western Hemlock, Western Spruce	2.5 - 4.2
Southern Hardwood	1.2 - 1.4
Northern Hardwood	1.0 - 1.2
<i>Eucalyptus</i>	0.8 - 1.0
White Oak	0.59
Sweetgum	0.48
Aspen	0.35

Eucalyptus trees represent the largest sources of fibres used globally in the paper industry (Bamber 1985; Ranatunga, 1964), and world-wide, there are an estimated ten to fifteen million hectares of land planted with *Eucalyptus* (Verhaegen and Plomion 1996). The major advantage of *Eucalypts* is their very high growth rates and ability to grow in a wide range of conditions, both tropical and temperate.

However, *Eucalyptus* fibres are significantly shorter than those from other, once more popular, sources of fibre such as pine. Thus papers that are made from *Eucalyptus* pulp are often weak and usually require reinforcement with longer fibres from other sources increasing the production costs. If trees could be produced with longer fibres, this would be a considerable advantage to the paper industry, increasing the quality of the raw materials for pulp and paper synthesis.

Through tree breeding it is possible to achieve some modification of fibre characteristics. For example, interspecific triploid hybrids of poplar have been developed which have longer fibres than the parental species.

Genetic variation in fibre properties is also evident within species. Fibre characteristics are controlled by a complex set of genetic factors and are not easily amenable to classical breeding methods. Therefore, existing genetic variation has not been exploited significantly in tree breeding programmes. Whilst knowledge is now being accumulated on the heritability of wood properties, previously these were not often considered as important as growth characteristics and were sometimes sacrificed in pursuit of the latter. In some instances, growth rate is negatively correlated with fibre characteristics, though this does not always hold true (e.g. in Eucalypts), and breeding efforts are now being made to capture the benefits of both.

In many cases fibre properties are sufficient for the end product, and improvement is considered unnecessary. For example, increasing fibre length beyond 2mm causes little increase in tear strength or tensile strength, and many softwood fibres are commonly around 3mm long, i.e. greater than the minimum for desired strength. However, fibres in juvenile wood tend to be shorter and there is an increased usage of juvenile material through a reduction in rotation times. Hence, there is scope for improvement even in those species which commonly yield long fibres.

From the perspective of the pulp and paper industry, fibres are specific types of plant cell walls that have been subjected to a range of treatments to remove all contents and most non-cellulosic wall components (Stewart et al, 1994). In woody plants the fibres are made up of dead cell wall material. In order to produce longer fibres it is necessary to have longer living cells during growth, before fibre formation.

The cell wall can be envisaged as a complex network of cellulose microfibrils linked together by noncovalent interactions with matrix polymers (Carpita and Gibeaut, 1993). The microfibrils are coated by a mixture of hemicelluloses which form extensive hydrogen-bonded interactions with the surface of the microfibrils. Coextensive with this is another network formed from various pectins which are held together largely by ionic linkages (McQueen-Mason, 1995).

To allow cells to grow and enlarge the wall components must loosen to enable slippage of the polysaccharides and proteins within the matrix (Cosgrove, 1993). Extension of the cell is then driven by the internal turgour pressure of the cell, which is considerable. The degree of extension during cell growth is controlled by the mechanical properties of the cell wall, which result from their composition and from the orientation of wall fibrils and structural polymers.

The control of cell wall extension is closely regulated by the plant to facilitate growth control and morphogenesis. The ultimate agents of control are enzymes located in the wall

itself. If plants express cell wall "loosening" enzymes in their walls, then it seems likely that these enzymes can regulate cell growth. Altered levels of expression can thereby cause increased or reduced cell growth and fibre length. Changes in cell wall texture may also be produced.

One class of cell wall proteins are the Expansins. Expansins induce the extension of plant walls, and at present are the only proteins reported with demonstrated wall-loosening activity. Expansins were first isolated from cucumber hypocotyl cell walls by McQueen-Mason et al (1992) and characterised by their ability to catalyse wall loosening in an *in vitro* rheological assay.

The mode of action of expansins is believed to be by weakening the noncovalent bonding between the cellulose and hemi-cellulose, with the result that the polymers slide relative to one another in the cell wall (Cosgrove 1996). The precise biochemical action of expansins is unclear, although it is known that their effects are not due to exoglycanase or xyloglucan endotransglycosylase activity (McQueen-Mason et al, 1992, McQueen-Mason & Cosgrove, 1993). Expansins appear to disrupt hydrogen bonding between cellulose microfibrils and hemicelluloses. The process enables wall loosening without any degradation of the polymers or an overall weakening of wall structure during expansion. Consistent with this mechanism, expansins have been shown to weaken cellulosic paper, which derives its mechanical strength from hydrogen bonding between cellulose fibres (McQueen-Mason and Cosgrove, 1994).

Expansins are able to restore the ability of isolated cell walls to extend in a pH dependent manner (McQueen-Mason and Cosgrove, 1995) and may be responsible for the phenomenon of "acid growth" in plants (Shcherban et al, 1995). Expansin proteins have been characterised in cucumber hypocotyls (McQueen-Mason et al, 1992), oat coleoptiles (Li et al, 1993), expanding tomato leaves (Keller and Cosgrove, 1995) and rice internodes (Cho and Kende, 1997).

Expansin cDNAs have been isolated and characterised from a number of plants and it is now evident that expansins exist as a multi-gene family showing a high level of conservation between species. cDNAs with high degrees of homology have been identified from collections of anonymous Expression Sequence Tag (EST) cDNAs from *Arabidopsis* and rice. These EST cDNAs exhibit a high degree of homology at the level of protein sequence (60-87%) indicating that expansin structure is highly conserved (Shcherban et al 1995). Expansins show no sequence similarity to other known enzymes, although they do have sequence similarities to some pollen allergens (Shcherban et al, 1995). Recently Cosgrove et al (1997) have shown that pollen allergens from maize also possess considerable expansin activity.

If plants can be modified to over-express expansins in their walls, then it seems likely that these plants will exhibit a marked increase in cell extension or growth. Conversely, a reduction in the expression of expansins should lead to a reduction in cell growth.

One approach to modifying the expression of expansins is via the introduction of recombinant DNA sequences into the plant genome. Several methods can be used to introduce foreign DNA into plant cells (see review by Weising et al, 1988; Miki and Iyer, 1990 and Walden 1994). *Agrobacterium tumefaciens*-mediated gene transfer is probably the most widely used and versatile of these methods (Walden, 1994).

Genetic modification experiments directed towards changing the wood and paper quality of trees has been investigated by other workers, particularly focusing on the lignin pathway in cells and lignin content in the final paper product (Hawkins and Boudet, 1994; Grima-Pettenati, et al, 1993; Poeydomenge et al, 1993; Boudet et al, 1995 and Hibino et al, 1994). The aim of the present invention differs in that it seeks to provide a means of controlling fibre growth and cell wall morphology.

An object of the present invention is to provide a method whereby trees can be modified to produce fibres of a desired length for specific applications. This will enable the forester to control the quality of his product. In addition it will enable the forester to produce a wide range of fibre types from a single or small number of species which can be selected as being ideally suited for cultivation in that particular site. This will result in both the economy of employing a single uniform silvicultural regime, and the flexibility of producing which ever type of fibre is required at a particular time.

The invention also provides a means of producing fibre of specific type from trees at particular periods in their growth cycle. For example, the production of long fibres from juvenile trees can be achieved, thereby accelerating the time to harvest of the crop.

This is achieved by firstly isolating and characterising expansin gene sequences from heterologous and homologous species and then reintroducing these genes into trees so as to alter expansin levels in the transgenic trees using over-expression, co-suppression and anti-sense knockout strategies. This will lead to the cultivation of trees more suitable for paper production.

The present invention provides a nucleic acid coding sequence encoding a gene capable of modifying the extension of fibre cell walls, the nucleic acid coding sequence being one or more of SEQ.ID. Nos. 1-6 hereof.

The present invention also provides a method of transforming trees to modify the fibre characteristics in trees, the method comprising stably incorporating into the plant genome a chimaeric gene comprising a promoter, a nucleic acid coding sequence encoding a gene capable of modifying the extension of fibre cell walls, and a terminator, and regenerating a plant having an altered genome.

The present invention also provides trees having therein a chimaeric gene comprising a promoter, a nucleic acid coding sequence capable of modifying the extension of fibre cell walls and a terminator.

Constructs and chimaeric genes having the DNA structural features described above are also aspects of the invention.

Plant cells containing chimaeric genes comprising a nucleic acid coding sequence capable of modifying the extension of fibre cell walls are also an aspect of this invention, as is the seed of the transformed plant containing chimaeric genes according to the invention.

The chimaeric gene may comprise the nucleic acid coding sequence as it exists in the genome, complete with endogenous promoter, terminator, introns and other regulatory sequences, or the nucleic acid coding sequence, with or without introns, may be combined with a heterologous promoter, terminator and/or other regulatory sequences.

The promoter may be a constitutive promoter, such as the cauliflower mosaic virus 35S gene or nopaline synthase promoter, a tissue specific promoter, such as rolC or an inducible promoter, such as AlcR/AlcS. Other suitable promoters will be known to those skilled in the art.

The nucleic acid sequence, or parts thereof, may be arranged in the normal reading frame direction, i.e. sense, or in the reverse reading frame direction, i.e. antisense. Up or down regulation of the activity of the expansin or expansin gene using sense, antisense or co-suppression technology may be used to achieve alteration in the length of fibre cell walls.

Preferably the nucleic acid sequence encodes one or more of the class of proteins known as expansins. The nucleic acid sequence may advantageously be one or more of SEQ. ID. Nos. 1-

6 hereof. Alternatively, the nucleic acid sequence may be a sequence which has sufficient homology to hybridise to any one of SEQ. ID. Nos. 1-6 under medium stringency conditions (washing at 2x SSC at 65°C).

Preferably the nucleic acid sequence is an mRNA or cDNA sequence, although it may be genomic DNA.

Preferably the nucleic acid sequence is derived from *Eucalyptus* or cucumber.

Trees which may suitably be transformed using the inventive method include Eucalypts, Aspen, pine, larch.

The nucleic acid sequence may be introduced by any of the known genetic transformation techniques such as *Agrobacterium tumefaciens* mediated transformation, *Agrobacterium rhizogenes* mediated transformation, biolistics, electroporation, chemical poration, microinjection or silicon-fibre transformation, for example.

In order that the invention may be easily understood and readily carried into effect, reference will now be made, by way of example, to the following Figures, in which:-

Figure 1a is a diagrammatic representation of the coding sequence for cucumber Ex29 cloned between the cauliflower mosaic virus 35S promoter and nos terminator in the vector pDE326;

Figure 1b is a diagrammatic representation showing the insert from Figure 1 between the EcoR I and Hind III restriction sites introduced into a modified Ti plasmid pDE 1001 to produce pDE/EXP29, and

Figure 1c is a diagrammatic representation showing the insert from Figure 1 between the EcoR I and Hind III restriction sites introduced into a modified Ti plasmid p35GUSINT to produce pATC/EXP29;

MATERIALS AND METHODS

RNA Extraction and mRNA Isolation:

RNA extraction from cucumber hypocotyls. Seeds of cucumber (*Cucumis sativus* L., cv Burpee pickler, from A.W. Burpee, Westminster, Penn, USA) were sown on water-soaked capillary matting (Fordingbridge Growers Supplies, Arundel, W. Sussex, UK) in plastic trays (35cm x 25cm x 6cm) and germinated in the dark at 27°C. After 4 days the etiolated seedlings were harvested under green light by excising the upper 20mm of the hypocotyl into liquid nitrogen and grinding to a fine powder in a pestle and mortar that had previously been chilled at -80°C. Total RNA was extracted in a hot phenol/lithium chloride buffer according to the procedure of Verwoerd et al (1989).

RNA extraction from *Eucalyptus grandis*. *E. grandis* seeds were sown on trays (35cm x 25cm x 6cm) of Levington's F2 compost (Levington Horticulture Ltd., Ipswich, Suffolk, UK) and germinated in a greenhouse (18-24°C, at a light intensity of approximately 10,000 lux, and 16 hours of daylight). After 8 weeks the seedlings were transferred to individual pots, and then repotted as necessary (approximately every 6-7 weeks). Growing stem tissue was harvested from the last 40-50mm of branch tips into liquid nitrogen. Immature leaves, usually

the youngest two from growing branch tips, were also harvested directly into liquid nitrogen; roots were washed in several bowls of tap water, rinsed with distilled water and then growing tips were excised into liquid nitrogen. RNA was extracted as described by Pawlowski et al (1994) using a protocol especially modified for the extraction of RNA from plants containing high levels of phenolic compounds.

Poly(A⁺) mRNA isolation from total RNA extracted from *E.grandis* stem tissue. Poly(A⁺) mRNA was isolated from total RNA using either push (Stratagene, Cambridge, UK) or spin oligo(dt) columns (Clontech Laboratories, Inc. CA., USA) and following the supplier's instructions and recommendations.

RT-PCR and Sequencing

The nucleic acid sequence of expansins show a considerable extent of divergence. However two regions with a reasonable degree of consensus were identified and used to synthesise two oligonucleotide primers of low complexity.

Total RNA was extracted from young stem tissue and Poly(A⁺) mRNA isolated using oligo(dt) columns as described above. 1µg of mRNA was used in a PCR experiment (50°C annealing temperature, 30 cycles, hot start) with the two expansin consensus primers (see Table 2) and Taq DNA polymerase (Promega UK Ltd.).

Table 2Sequence of Consensus Expansin Primers

	Sequence (5'-3')
P.1 (SEQ. ID. No. 7)	ATGGIGGIGCNTGYGGNTA
P.2 (SEQ. ID. No. 8)	TGCCARTTYTGNCCCCARTT
Key: Y=C or T, N=A or G or C or T, R=A or G, I=Inosine	

cDNA Library Construction

For first strand cDNA synthesis 1 μ g of mRNA was used in a reaction with 0.15 μ g OG1 oligo dt primers and AMV Reverse Transcriptase (9 units/ μ l, Promega UK Ltd., Southampton, UK).

The library was constructed in the Lambda ZAP II vector (Stratagene, Cambridge, UK), following the supplier's instructions.

Northern Analysis

Total RNA was isolated from the stem, leaves and roots of *E. grandis* as described above. 6 μ g of RNA in 20 μ l DEPC H₂O was denatured in a equal volume of denaturing solution (50% formamide, 2x TBE) and run on a standard 1.5% agarose gel at 75 volts for 200 min. RNA from the gel was transferred onto "Zeta-Probe" GT Genomic Tested Blotting Membranes (Biorad Laboratories, California, USA) by capillary transfer. Partial *E.grandis* expansin sequences generated by RT-PCR from stem mRNA (as described above) were used for 32P-random prime labelling and hybridised to the transferred RNA following the membrane supplier's recommended methods (Biorad Laboratories).

Vector Construction

The coding sequence for cucumber Ex29 (GenBank Accession No. U30382; known as Cs-EXP1, and Shcherban et al 1995) was generated by RT-PCR and cloned between the Cauliflower Mosaic Virus 35S promoter and *nos* terminator (see Figure 1a) into pDE326, a vector kindly donated by Dr. Jürgen Denecke of York University. After insertion of the Ex29 expansin sequence the inserts were sequenced to check for correct in frame insertion by sequencing using a primer located within the 35S promoter region.

Inserts containing the 35S promoter, Ex29 sequence and *nos* terminator were cut between the *EcoRI* and *HindIII* restriction sites and inserted into modified Ti plasmids to produce transformation constructs. Two modified Ti plasmids were used: pDE1001 (Denecke et al, 1992 or Shcherban et al 1995) provided by Dr. Jürgen Denecke and p35GUSINT (Vancanneyt et al, 1990). The plasmids containing the insert were referred to as pDE/EXP29 (pDE1001 + Ex29) (see Figure 1b) and pATC/EXP29 (p35GUSINT + Ex29) (See Figure 1c), acknowledging the source of the plasmids. Plasmids were transferred into *E.coli* by standard procedures; *E.coli* strains were grown on LB plates (incubated at 37°C and stored at 4°C) or in LB medium with the appropriate antibiotic for positive selection.

Two strains of *Agrobacterium tumefaciens* were used. A C58 strain (C58C1(pGV2260) Deblaere, R. et al 1985) kindly donated by Dr. Jürgen Denecke, and EHA105 deposited by Advanced Technologies (Cambridge) Limited of 210 Cambridge Science Park, Cambridge CB4 4WA, under the Budapest Treaty on

the International Recognition of the Deposit of Micro-organisms for the purposes of Patent Procedure at the National Collection of Industrial and Marine Bacteria (NCIMB), 23 St. Machar Street, Aberdeen, Scotland on 25 August 1998 under Accession No. NCIMB 40968. *Agrobacterium* were grown on LB plates (incubated at 27°C and stored at 4°C) or in LB medium with the appropriate antibiotic for positive selection. The constructs were introduced into *Agrobacterium* via direct DNA transformation or by tri-parental mating using the *E.coli* mobilisation function strain HB101 (pRK2013) (Figurski and Helinski 1979)

Plant Transformation

Young leaves were dissected under sterile conditions, from approximately 4 week old *E.grandis* cultures grown in Magenta boxes (7cm x 7cm x 13cm) on LS media at 25°C, in a growth room in our tissue culture laboratory and used for *Agrobacterium*-mediated infection (Horsch, Fry, Hoffman, Eichholtz, Rogers, and Fraley 1985). Inoculated tissue was left to co-cultivate for 4d on LS media (plus 20g/l glucose, 0.7% agarose, 0.01mM Zeatin a 1μM NAA) in diffuse light in a growth room, conditions as before. Transformants were selected on 50mg/l kanamycin and 250mg/l claforan.

RESULTS

Isolation of Novel Expansin Sequences from *E.grandis* stem tissue

Using the methods described, transformed pTAG clones were isolated by blue-white colony selection on agar plates following the methods described by the supplier (R&D Systems). Twenty white ("positive") colonies were selected and sequenced. Of these, six were identified as containing sequences that had similarities with other known expansin sequences using a basic BLAST search provided by NCBI. The putative transcripts were all around 450 bps in size (determined by PCR and gel electrophoresis). PCR products were sequenced using a forward primer and the sequences identified as SEQ.ID. Nos. 1-6 were obtained.

Vector Construction and Plant Transformation

As described in the Methods two constructs for plant transformation were prepared and introduced into two strains of *Agrobacterium*, C58 and EHA 105 to produce C58 containing pDE + Ex29, C58 containing pATC + Ex29 and EHA105 containing pATC + Ex29. Each construct-containing strain was used to inoculate 400 leaves dissected from *E.grandis* tissue (on two separate occasions, each time inoculating 200 leaves).

The transformation experiments were repeated with a further 240 leaves, inoculated with EHA105 containing pATC + Ex29 to increase the amount of possible transformants obtainable.

From the original batch of inoculated tissue with EHA105, 25 plants were grown in the greenhouse and the properties of the shoots determined.

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(C) CITY: Staines
(D) STATE: Middlesex
(E) COUNTRY: England
(F) POSTAL CODE: TW18 1DY

(ii) TITLE OF INVENTION: Modification of Plant Fibres

(iii) NUMBER OF SEQUENCES: 6

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(D) STATE: Hampshire
(E) COUNTRY: England
(F) POSTAL CODE: SO15 8TL

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette 3.50 inch
(B) COMPUTER: Viglen P5/75
(C) OPERATING SYSTEM: MS-DOS Windows 95
(D) SOFTWARE: Microsoft Word 97

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: Not yet known
(C) CLASSIFICATION: Not yet known

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE: RD-ATC-19

(ix) TELECOMMUNICATION INFORMATION:

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(B) TELEFAX: 01703 779856

INFORMATION FOR SEQUENCE ID. NO. 1

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	488 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	double
(D)	TOPOLOGY	linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Eucalyptus grandis*

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO. 1

ATGGGGGGGG	CTTGTGGGTA	TGGCAACCTG	TACAGCCAAG	GCTATGGCAC	50
CAACACTGCA	GCTTTGAGCA	CTGCCCTGTT	CAACAATGGC	CTGAGCTGCG	100
GGGCATGTTA	CGAGATGCGG	TGCAACGACG	ACCCAGGTG	GTGCCTCCCG	150
GGGACCATCA	TGGTCACGGC	AACCAACTTT	TGCCCTCCCA	ACTTGGCCCT	200
CTCCAACGAC	AATTGCGGCT	GGTGCAACCC	CCCTCTCCAG	CACTTCGATA	250
TGGCCGAGCC	TGCTTTCTTG	CAGATTGCCC	AGTACAAAGC	TGGGATTGTC	300
CAGGTTTCCT	TCAGAAGGGT	TCCGTGTGTG	AAGAAAGGAG	GGGTAAGGTT	350
CACCATCAAT	GGGCACTCCT	ACTTCAACTT	GGTGCTGATC	ACCAACGTGG	400
GAGGTGCTGG	TGATGTCCAT	TCCGTTTCCA	TCAAGGGCTC	GAGGACTGGT	450
TGGCAAGCCA	TGTCAAGGAA	CTGGGGCAAA	AACTGGCA		488

INFORMATION FOR SEQUENCE ID. NO. 2

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	475 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	double
(D)	TOPOLOGY	linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Eucalyptus grandis*

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO. 2

ATGGGGGGGG	CATGCGGGTA	TGGCAACCTG	TACAGCCAAG	GCTATGGCAC	50
CAACACTGCA	GCTTTGAGCA	CTGCCCTGTT	CAACAATGGC	CTGAGCTGCG	100
GGGCATGTTA	CGAGATGCGG	TGCAACGACG	ACCCCAGGTG	GTGCCTCCCG	150
GGGACCATCA	TGGTCACGGC	AACCAACTTT	TGCCCTCCCA	ACTTGGCCCT	200
CTCCAACGAC	AATGGCGGCT	GGTGCAACCC	CCCTCTCCAG	CACTTCGATA	250
TGGCCGAGCC	TGCTTTCTTG	CAGATTGCCC	AGTACAAAGC	TGGGATTGTC	300
CCGGTTTCCT	TCAGAAGGGT	TCCGTGTGTG	AAGAAAGGAG	GGGTAAGGTT	350
CACCATCAAT	GGGCACTCCT	ACTTCAGCTG	TGGTGCTGAT	CACCAACGTG	400
GGAGGTGCTG	GTGATGTCCA	TTCCGTTTCC	ATCAAGAGCT	CGAGGACTGG	450
TTGGCAAGCC	ATGTCAAGGA	ATTGA			475

INFORMATION FOR SEQUENCE ID. NO. 3

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	494 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	double
(D)	TOPOLOGY	linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Eucalyptus grandis*

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO. 3

ATGGGGGGGG	CATGTGGTTA	CGGGGACCTT	CACAGGGCCA	CCTATGGCAA	50
GTACAGTGCC	GGCTTGAGCT	CGATGCTGTT	CAACAGAGGG	AGTACCTGCG	100
GGGCTTGCTT	CGAGCTCCGG	TGCGTCGACC	ACATTTTGTG	GTGCCTCCCT	150
GGTAGCCCGT	CGGTGATCCT	CACCGCCACC	GACTTCTGCC	CTCCGAACTA	200
CGGGCTCGCG	GCAGATTACG	GCGGGTGGTG	CAACTTCCCG	CAGGAGCACT	250
TCGAGATGTC	GGAGGCGGCC	TTCGCCGAGA	TTGCGGTGCG	AAGGGCTGAT	300
GTGGTGCCTA	TCCAGTACAG	GAGGGTGAAC	TGTCTGAGAA	GCGGTGGTCT	350
GAGATTCACA	TTGAGCGGAA	ACTCTCACTT	CTTTCAGGTC	TTGGTGACGA	400
ATGTAGGCCT	AGATGGGGAG	GTGATTGCCA	TGAAAATGAA	GGGATCGAAA	450
ACAGGGTGGA	TACCGATGGC	AAGAAACTGG	GGCAAAAAC	GGCA	494

INFORMATION FOR SEQUENCE ID. NO: 4

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	437 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	double
(D)	TOPOLOGY	linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Eucalyptus grandis

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO. 4

ATGGGTTGCC ACCGGGTCCT TGATCCTTTG ATGGCCACGG AGTGCACATC	50
CCCTGCTCCG CCGACATTGG TTATGAGCAC GAGGTTGAAA TAAGAATGGC	100
CGTTGACGGT GAACCGGATC CCTCCGCTTC TCCTGCACCT CACTCTTCGG	150
TAGGCCACCG GGACGATCCC GGCCCTGTAC TGCGCAATGT GCTGGAAGAC	200
CGGCTGGGAG AGGTCGAAAT GGAGTTGAGG AGGGTCGCAC CACCCTCCTG	250
GAGGGCAGAA GTTGGTCGCC GTGACCACAA TGGCGCCCGG GAGGCACCAC	300
TGCGGGTCGT TCACGCACCG GAGCTCAAAG CACGCGCCGC AGCTCAGCCC	350
ATTGTTGAAC AATGCAGTGC TCAGTGCAGC TGTGTTTGTG CCGTACCCTT	400
GGCTGTATAG ATTCCCATAA CCACACGCCC CCCCCAT	437

INFORMATION FOR SEQUENCE ID. NO: 5

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	437 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	double
(D)	TOPOLOGY	linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Eucalyptus grandis*

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO. 5

ATGGGTTGCC ACCGGGTCCT TGATCCTTTG ATGGCCACGG AGTGCACATC	50
CCCTGCTCCG CCGACATTGG TTATGAGCAC GAGGTTGAAA TAAGAATGGC	100
CGTTGACGGT GAACCGGATC CCTCCGCTTC TCCTGCACCT CACTCTTCGG	150
TAGGCCACAG GGACGATCCC GGCCCTGTAC TGCGCAATGT GCTGGAAGAC	200
AGGCTGGGAG AGGTCGAAAT GGAGTTGAGG AGGGTCGCAC CACCCTCCTG	250
GAGGGCAGAA GTTGGTCGCC GTGACAACAA TGGCGCCCGG GAGGCACCAC	300
TGCGGGTCGT TCACGCACCG GAGCTCAAAG CACGCGCCGC AGCTCAGCCC	350
ATTGTTGAAC AATGCAGTGC TCAGTGCAGC TGTGTTTGTG CCGTACCCTT	400
GGCTGTATAG ATTCCCATAA CCACACGCCC CCCCCAT	437

INFORMATION FOR SEQUENCE ID. NO: 6

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	448 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	double
(D)	TOPOLOGY	linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Eucalyptus grandis*

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO. 6

CCTTGACATG GTCTGCCACC TTGTCCGCGA ACCCTTCACG GCGACCGAGT	50
TGACGTTGCC TGCGCCGCCG ACGTTTGTGA CGAGGACGAG CTTGAAGTAT	100
GAGTTGCCGT TGATGGTGAA CCGGATGCCT CCTCTCCTCC TGCACGTCAC	150
CCTCCTGTAC GCAACGTGGA CGATGCCGGC TCGGTACTTG GCAATGTGCT	200
GGAAGACGGG CTGGGAGATG TCGAAGTGGT GTTGGGGCGG GTTGCACCAT	250
CCGCCGGCGT TGTTTGGGAG GGC GTTGT TT GGCGGGCAGA AGTTTGTGGC	300
GGTGACGACG ATGGAGCCGC CCAGGCACCA CTTTCCGTCG TTCACGCACC	350
GGATCTCGAA GCACGACCCC CAGCTCAGCC CGTTTTTTTAA CAGCGCCGTG	400
CTCAGCGCCG CCGTGTTTCGT ACCGTAGCCC TGGCTGTACA GGTTGCCG	448

INFORMATION FOR SEQUENCE ID. NO. 7

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	19 nucleotides
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY	linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO. 7

ATGGIGGIGC NTGTGGNTA

19

Key I = Inosine
N = A, G, T or C

INFORMATION FOR SEQUENCE ID. NO: 8

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	20 nucleotides
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY	linear

(ii) MOLECULE TYPE: Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO. 6

TGCCARTTYT GNCCCCARTT

20

Key R = A or G
Y = T or C
N = A, G, T or C

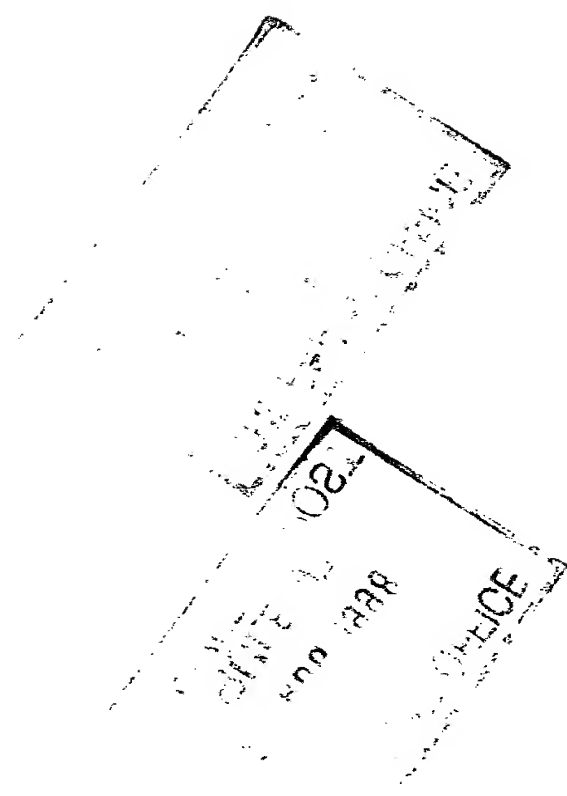
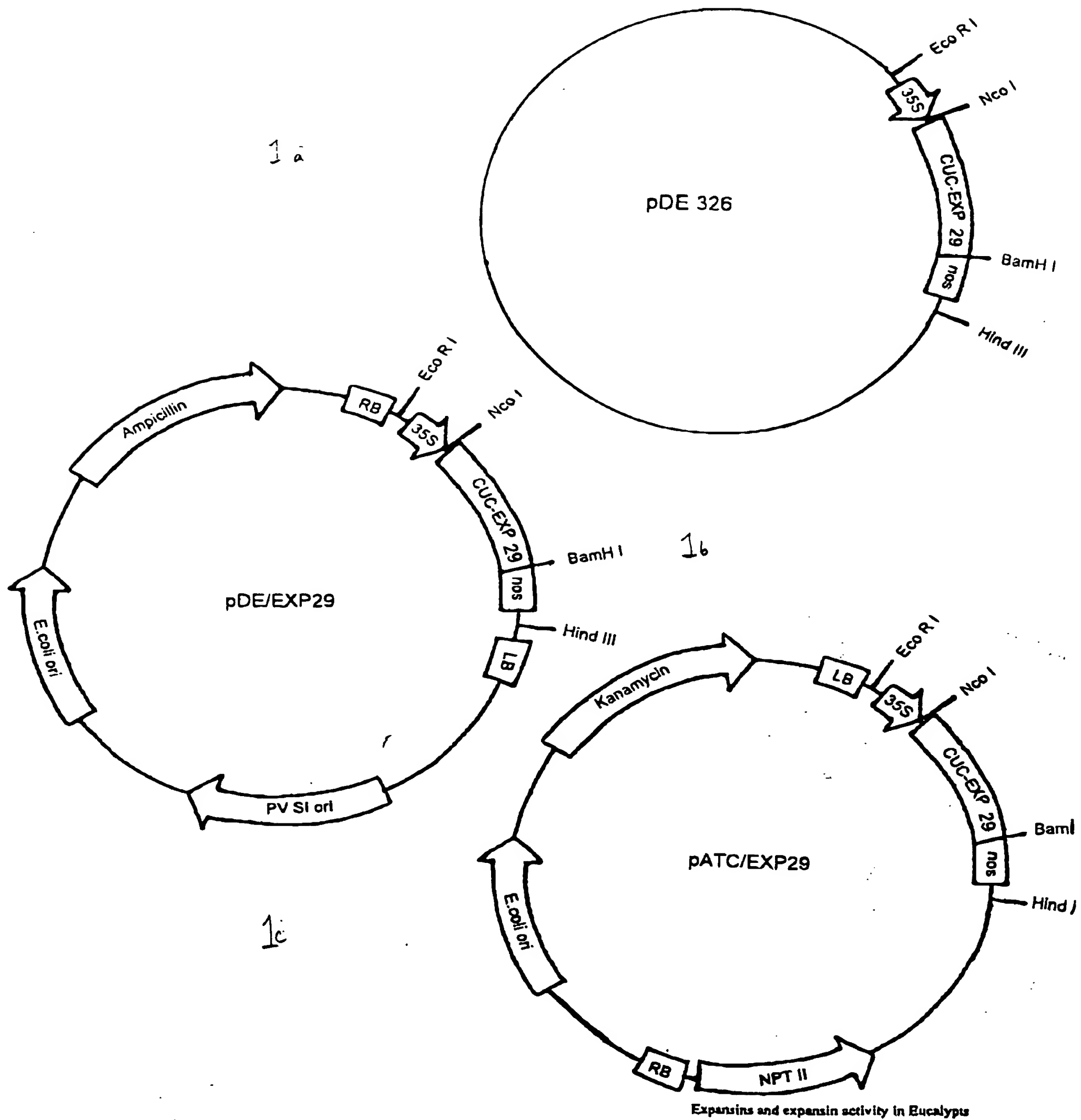


Figure 22 Diagram of Constructs prepared for Plant Transformation:
C58/pDE, C58/pATC and EHA105/pATC.



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